RAW SEQUENCE LISTING

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Application Serial Number: _/0/048,116β_

Source: _1Fw16_

Date Processed by STIC: _4/20/06_

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        RAW SEQUENCE LISTING              DATE: 04/20/2006
        PATENT APPLICATION:  US/10/048,116B    TIME: 09:51:03

        Input Set : A:\seq list.txt
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 3 <110> APPLICANT: CNRS
 5 <120> TITLE OF INVENTION: RECOMBINANT PROTEINS AND MOLECULAR COMPLEXES DERIVED
 6       FROM THESE PROTEINS, ANALOGOUS TO MOLECULES INVOLVED IN
 7       IMMUNE RESPONSES
 9 <130> FILE REFERENCE: 1721-47
11 <140> CURRENT APPLICATION NUMBER: 10/048,116B
12 <141> CURRENT FILING DATE: 2002-02-27
14 <150> PRIOR APPLICATION NUMBER: PCT/FR00/02193
15 <151> PRIOR FILING DATE: 2000-07-28
17 <150> PRIOR APPLICATION NUMBER: FR99/09862
18 <151> PRIOR FILING DATE: 1999-07-29
20 <160> NUMBER OF SEQ ID NOS: 8
22 <170> SOFTWARE: PatentIn Ver. 2.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1517
26 <212> TYPE: DNA
27 <213> ORGANISM: Artificial Sequence
29 <220> FEATURE:
30 <223> OTHER INFORMATION: Description of Artificial Sequence: construct
31       coding IAalpha(d)/Fc
33 <220> FEATURE:
34 <221> NAME/KEY: CDS
35 <222> LOCATION: (18)..(1502)
37 <400> SEQUENCE: 1
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39                     Met Pro Cys Ser Arg Ala Leu Ile Leu Gly Val
40                      1               5                   10
42 ctc gcc ctg aac acc atg ctc agc ctc tgc gga ggt gaa gac gac att      98
43 Leu Ala Leu Asn Thr Met Leu Ser Leu Cys Gly Gly Glu Asp Asp Ile
44             15                  20                  25
46 gag gcc gac cac gta ggc ttc tat ggt aca act gtt tat cag tct cct     146
47 Glu Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro
48         30                  35                  40
50 gga gac att ggc cag tac aca cat gaa ttt gat ggt gat gag ttg ttc     194
51 Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe
52     45                  50                  55
54 tat gtg gac ttg gat aag aag aaa act gtc tgg agg ctt cct gag ttt     242
55 Tyr Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg Leu Pro Glu Phe
56 60                  65                  70                  75
58 ggc caa ttg ata ctc ttt gag ccc caa ggt gga ctg caa aac ata gct     290
59 Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala
60                 80                  85                  90
62 gca gaa aaa cac aac ttg gga atc ttg act aag agg tca aat ttc acc     338
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63 Ala Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr
64          95              100              105
66 cca gct acc aat gag gct cct caa gcg act gtg ttc ccc aag tcc cct     386
67 Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro
68          110              115              120
70 gtg ctg ctg ggt cag ccc aac acc ctt atc tgc ttt gtg gac aac atc     434
71 Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile
72     125              130              135
74 ttc cca cct gtg atc aac atc aca tgg ctc aga aat agc aag tca gtc     482
75 Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val
76 140              145              150              155
78 aca gac ggc gtt tat gag acc agc ttc ctc gtc aac cgt gac cat tcc     530
79 Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser
80              160              165              170
82 ttc cac aag ctg tct tat ctc acc ttc atc cct tct gat gat gac att     578
83 Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile
84              175              180              185
86 tat gac tgc aag gtg gag cac tgg ggc ctg gag gag ccg gtt ctg aaa     626
87 Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys
88          190              195              200
90 cac tgg gaa cct gag att cca gcc ccc atg tca gag ctg aca gaa act     674
91 His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr
92     205              210              215
94 gga ggt gga gga tcc act aca gct cca tca gct cag ctc gaa aaa gag     722
95 Gly Gly Gly Gly Ser Thr Thr Ala Pro Ser Ala Gln Leu Glu Lys Glu
96 220              225              230              235
98 ctc cag gcc ctg gag aag gaa aat gca cag ctg gaa tgg gag ttg caa     770
99 Leu Gln Ala Leu Glu Lys Glu Asn Ala Gln Leu Glu Trp Glu Leu Gln
100              240              245              250
102 gca ctg gaa aag gaa ctg gct cag gca gca tct gag ccc aga ggg ccc     818
103 Ala Leu Glu Lys Glu Leu Ala Gln Ala Ala Ser Glu Pro Arg Gly Pro
104              255              260              265
106 aca atc aag ccc tgt cct cca tgc aaa tgc cca gca cct aac ctc ttg     866
107 Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu
108          270              275              280
110 ggt gga cca tcc gtc ttc atc ttc cct cca aag atc aag gat gta ctc     914
111 Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu
112     285              290              295
114 atg atc tcc ctg agc ccc ata gtc aca tgt gtg gtg gtg gat gtg agc     962
115 Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser
116 300              305              310              315
118 gag gat gac cca gat gtc cag atc agc tgg ttt gtg aac aac gtg gaa     1010
119 Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu
120              320              325              330
122 gta cac aca gct cag aca caa acc cat aga gag gat tac aac agt act     1058
123 Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr
124              335              340              345
126 ctc cgg gtg gtc agt gcc ctc ccc atc cag cac cag gac tgg atg agt     1106
127 Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser
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Input Set : **A:\seq list.txt**
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128         350                    355                    360
130 ggc aag gag ttc aaa tgc aag gtc aac aac aaa gac ctc cca gcg ccc    1154
131 Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro
132     365                    370                    375
134 atc gag aga acc atc tca aaa ccc aaa ggg tca gta aga gct cca cag    1202
135 Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln
136 380                    385                    390                    395
138 gta tat gtc ttg cct cca cca gaa gaa gag atg act aag aaa cag gtc    1250
139 Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val
140                     400                    405                    410
142 act ctg acc tgc atg gtc aca gac ttc atg cct gaa gac att tac gtg    1298
143 Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val
144             415                    420                    425
146 gag tgg acc aac aac ggg aaa aca gag cta aac tac aag aac act gaa    1346
147 Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu
148         430                    435                    440
150 cca gtc ctg gac tct gat ggt tct tac ttc atg tac agc aag ctg aga    1394
151 Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg
152     445                    450                    455
154 gtg gaa aag aag aac tgg gtg gaa aga aat agc tac tcc tgt tca gtg    1442
155 Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val
156 460                    465                    470                    475
158 gtc cac gag ggt ctg cac aat cac cac acg act aag agc ttc tcc cgg    1490
159 Val His Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg
160             480                    485                    490
162 act ccg ggt aaa tgatgactcg acctg                                   1517
163 Thr Pro Gly Lys
164             495
167 <210> SEQ ID NO: 2
168 <211> LENGTH: 495
169 <212> TYPE: PRT
170 <213> ORGANISM: Artificial Sequence
172 <220> FEATURE:
173 <223> OTHER INFORMATION: Description of Artificial Sequence: construct
174         coding IAalpha(d)/Fc
176 <400> SEQUENCE: 2
177 Met Pro Cys Ser Arg Ala Leu Ile Leu Gly Val Leu Ala Leu Asn Thr
178   1               5                   10                  15
180 Met Leu Ser Leu Cys Gly Gly Glu Asp Asp Ile Glu Ala Asp His Val
181             20                  25                  30
183 Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln
184         35                  40                  45
186 Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe Tyr Val Asp Leu Asp
187     50                  55                  60
189 Lys Lys Lys Thr Val Trp Arg Leu Pro Glu Phe Gly Gln Leu Ile Leu
190 65                  70                  75                  80
192 Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala Ala Glu Lys His Asn
193             85                  90                  95
195 Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr Pro Ala Thr Asn Glu
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196              100              105              110
198 Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln
199          115              120              125
201 Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile Phe Pro Pro Val Ile
202          130              135              140
204 Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr
205 145              150              155              160
207 Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser
208              165              170              175
210 Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile Tyr Asp Cys Lys Val
211          180              185              190
213 Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys His Trp Glu Pro Glu
214          195              200              205
216 Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr Gly Gly Gly Gly Ser
217          210              215              220
219 Thr Thr Ala Pro Ser Ala Gln Leu Glu Lys Glu Leu Gln Ala Leu Glu
220 225              230              235              240
222 Lys Glu Asn Ala Gln Leu Glu Trp Glu Leu Gln Ala Leu Glu Lys Glu
223                245                250              255
225 Leu Ala Gln Ala Ala Ser Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys
226              260              265              270
228 Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val
229          275              280              285
231 Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser
232          290              295              300
234 Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp
235 305              310              315              320
237 Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln
238              325              330              335
240 Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser
241          340              345              350
243 Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys
244          355              360              365
246 Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile
247          370              375              380
249 Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro
250 385              390              395              400
252 Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met
253              405              410              415
255 Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn
256              420              425              430
258 Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser
259          435              440              445
261 Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn
262          450              455              460
264 Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu
265 465              470              475              480
267 His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
268              485              490              495
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271 <210> SEQ ID NO: 3
272 <211> LENGTH: 1485
273 <212> TYPE: DNA
274 <213> ORGANISM: Artificial Sequence
276 <220> FEATURE:
277 <223> OTHER INFORMATION: Description of Artificial Sequence:coding region
278       of SEQ ID NO:1
280 <220> FEATURE:
281 <221> NAME/KEY: CDS
282 <222> LOCATION: (1)..(1485)
284 <400> SEQUENCE: 3
285 atg ccg tgc agc aga gct ctg att ctg ggg gtc ctc gcc ctg aac acc   48
286 Met Pro Cys Ser Arg Ala Leu Ile Leu Gly Val Leu Ala Leu Asn Thr
287  1               5                  10                  15
289 atg ctc agc ctc tgc gga ggt gaa gac gac att gag gcc gac cac gta   96
290 Met Leu Ser Leu Cys Gly Gly Glu Asp Asp Ile Glu Ala Asp His Val
291              20                  25                  30
293 ggc ttc tat ggt aca act gtt tat cag tct cct gga gac att ggc cag  144
294 Gly Phe Tyr Gly Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln
295              35                  40                  45
297 tac aca cat gaa ttt gat ggt gat gag ttg ttc tat gtg gac ttg gat  192
298 Tyr Thr His Glu Phe Asp Gly Asp Glu Leu Phe Tyr Val Asp Leu Asp
299      50                  55                  60
301 aag aag aaa act gtc tgg agg ctt cct gag ttt ggc caa ttg ata ctc  240
302 Lys Lys Lys Thr Val Trp Arg Leu Pro Glu Phe Gly Gln Leu Ile Leu
303  65                  70                  75                  80
305 ttt gag ccc caa ggt gga ctg caa aac ata gct gca gaa aaa cac aac  288
306 Phe Glu Pro Gln Gly Gly Leu Gln Asn Ile Ala Ala Glu Lys His Asn
307                  85                  90                  95
309 ttg gga atc ttg act aag agg tca aat ttc acc cca gct acc aat gag  336
310 Leu Gly Ile Leu Thr Lys Arg Ser Asn Phe Thr Pro Ala Thr Asn Glu
311              100                 105                 110
313 gct cct caa gcg act gtg ttc ccc aag tcc cct gtg ctg ctg ggt cag  384
314 Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln
315          115                 120                 125
317 ccc aac acc ctt atc tgc ttt gtg gac aac atc ttc cca cct gtg atc  432
318 Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile Phe Pro Pro Val Ile
319      130                 135                 140
321 aac atc aca tgg ctc aga aat agc aag tca gtc aca gac ggc gtt tat  480
322 Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr
323 145                 150                 155                 160
325 gag acc agc ttc ctc gtc aac cgt gac cat tcc ttc cac aag ctg tct  528
326 Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser
327                 165                 170                 175
329 tat ctc acc ttc atc cct tct gat gat gac att tat gac tgc aag gtg  576
330 Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile Tyr Asp Cys Lys Val
331              180                 185                 190
333 gag cac tgg ggc ctg gag gag ccg gtt ctg aaa cac tgg gaa cct gag  624
334 Glu His Trp Gly Leu Glu Glu Pro Val Leu Lys His Trp Glu Pro Glu
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VERIFICATION SUMMARY   DATE: 04/20/2006
PATENT APPLICATION: **US/10/048,116B**   TIME: 09:51:04

Input Set : **A:\seq list.txt**
Output Set: **N:\CRF4\04202006\J048116B.raw**